

SCORE Search Results Details for Application 10010742 and Search Result 20070109_163058_us-10-010-742-52.rng.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 02:40:48 ; Search time 418 Seconds
(without alignments)
6321.728 Million cell updates/sec

Title: US-10-010-742-52
Perfect score: 379
Sequence: 1 acttttgccaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379	100.0	379	4	AAH55527	Aah55527 Human bre
2	379	100.0	379	7	ADU01271	Adu01271 Breast ca
3	379	100.0	379	7	ADZ41535	Adz41535 Human bre
4	379	100.0	379	12	ADN40297	Adn40297 Human bre
c 5	379	100.0	397	4	AAL13663	Aal13663 Human bre
6	379	100.0	403	4	AAL18673	Aal18673 Human bre
c 7	379	100.0	598	5	ABV24442	Abv24442 Human pro
c 8	379	100.0	598	5	ABV28048	Abv28048 Human pro
c 9	379	100.0	870	11	ACN83733	Acn83733 Breast ca
c 10	379	100.0	963	7	ADU01522	Adu01522 Breast ca
c 11	379	100.0	963	7	ADZ41786	Adz41786 Human bre
c 12	379	100.0	1299	11	ACN89634	Acn89634 Breast ca
c 13	379	100.0	1518	7	ADU01524	Adu01524 Breast ca
c 14	379	100.0	1518	7	ADZ41788	Adz41788 Human bre
c 15	379	100.0	1518	12	ADQ48399	Adq48399 Human cyt
c 16	379	100.0	1586	4	AAD09946	Aad09946 Human dru
c 17	379	100.0	1598	7	ADU01521	Adu01521 Breast ca
c 18	379	100.0	1598	7	ADZ41785	Adz41785 Human bre
c 19	379	100.0	1743	12	ADJ67057	Adj67057 Human sec
c 20	379	100.0	1894	6	ABT07693	Abt07693 Breast ca
c 21	379	100.0	1906	12	ADQ36612	Adq36612 Human CYP
c 22	379	100.0	1975	10	AAD60551	Aad60551 Human cyt
c 23	379	100.0	1975	10	ACA61906	Aca61906 cDNA enco
c 24	379	100.0	1975	12	ADQ48397	Adq48397 Human cyt
c 25	379	100.0	2015	6	AAD24015	Aad24015 Human dru
c 26	379	100.0	2015	7	ADU01523	Adu01523 Breast ca
c 27	379	100.0	2015	7	ADZ41787	Adz41787 Human bre
c 28	379	100.0	2020	6	ABK33550	Abk33550 cDNA enco
c 29	379	100.0	2020	7	ADY31769	Ady31769 Novel hum
c 30	379	100.0	2020	8	ACA68511	Aca68511 Novel hum
c 31	379	100.0	2020	9	ABT44240	Abt44240 Human PRO
c 32	379	100.0	2020	9	ABT44523	Abt44523 Human PRO
c 33	379	100.0	2020	9	ACD82190	Acd82190 Human sec
c 34	379	100.0	2020	9	ABT43896	Abt43896 Human mem
c 35	379	100.0	2020	9	ADB83519	Adb83519 Novel hum
c 36	379	100.0	2020	9	ADB80625	Adb80625 Novel hum
c 37	379	100.0	2020	9	ADB73166	Adb73166 Novel hum
c 38	379	100.0	2020	9	ADB78248	Adb78248 Novel hum
c 39	379	100.0	2020	10	ADB84896	Adb84896 Human PRO
c 40	379	100.0	2020	10	ADB78002	Adb78002 Novel hum
c 41	379	100.0	2020	10	ADB87068	Adb87068 Human PRO
c 42	379	100.0	2020	10	ADB84650	Adb84650 Human PRO
c 43	379	100.0	2020	10	ADB83765	Adb83765 Novel hum
c 44	379	100.0	2020	10	ADB72920	Adb72920 Novel hum
c 45	379	100.0	2020	10	ADC36758	Adc36758 Human PRO

ALIGNMENTS

RESULT 1

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 02:47:13 ; Search time 2707 Seconds
(without alignments)
8953.111 Million cell updates/sec

Title: US-10-010-742-52
Perfect score: 379
Sequence: 1 actttgccaaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	379	100.0	379	2	CS110385	CS110385 Sequence
2	379	100.0	379	2	AX156195	AX156195 Sequence
c 3	379	100.0	397	2	CQ421094	CQ421094 Sequence
4	379	100.0	403	2	CQ426106	CQ426106 Sequence
c 5	379	100.0	598	2	CQ492564	CQ492564 Sequence
c 6	379	100.0	598	2	CQ496194	CQ496194 Sequence
c 7	379	100.0	963	2	CS110636	CS110636 Sequence
c 8	379	100.0	1518	2	CS110638	CS110638 Sequence
c 9	379	100.0	1548	2	CS110645	CS110645 Sequence
c 10	379	100.0	1586	2	AX195182	AX195182 Sequence
c 11	379	100.0	1598	2	CS110635	CS110635 Sequence
c 12	379	100.0	1894	2	AX829108	AX829108 Sequence
c 13	379	100.0	1907	5	AY262056	AY262056 Homo sapi
c 14	379	100.0	2015	2	CS110637	CS110637 Sequence
c 15	379	100.0	2015	2	AX317983	AX317983 Sequence
c 16	379	100.0	2020	2	CQ970464	CQ970464 Sequence
c 17	379	100.0	2020	2	AX358776	AX358776 Sequence
c 18	379	100.0	2020	2	AX362269	AX362269 Sequence
c 19	379	100.0	2020	5	AY358631	AY358631 Homo sapi
c 20	377.4	99.6	386	2	CQ430462	CQ430462 Sequence
c 21	377.4	99.6	393	2	CQ418480	CQ418480 Sequence
c 22	377.4	99.6	393	2	CQ421061	CQ421061 Sequence
c 23	377.4	99.6	393	2	CQ426250	CQ426250 Sequence
c 24	372	98.2	651	2	CQ421181	CQ421181 Sequence
c 25	369.4	97.5	792	2	CQ430054	CQ430054 Sequence
c 26	367	96.8	392	2	CQ429968	CQ429968 Sequence
c 27	365.4	96.4	392	2	CQ429935	CQ429935 Sequence
28	365.4	96.4	397	2	CQ421574	CQ421574 Sequence
29	363	95.8	393	2	CQ430100	CQ430100 Sequence
30	363	95.8	415	2	CQ421229	CQ421229 Sequence
c 31	363	95.8	1436	5	AY262057	AY262057 Homo sapi
c 32	363	95.8	2608	2	CS168612	CS168612 Sequence
c 33	363	95.8	2608	2	AX834733	AX834733 Sequence
c 34	363	95.8	2608	5	AK097373	AK097373 Homo sapi
c 35	361.4	95.4	392	2	CQ426196	CQ426196 Sequence
c 36	357.2	94.2	1503	2	AX768910	AX768910 Sequence
37	356	93.9	422	2	CQ418336	CQ418336 Sequence
c 38	342.4	90.3	357	2	CQ421595	CQ421595 Sequence
c 39	329.4	86.9	364	2	CQ426051	CQ426051 Sequence
c 40	317.6	83.8	391	2	CQ417373	CQ417373 Sequence
c 41	313.8	82.8	396	2	CQ418426	CQ418426 Sequence
42	312.4	82.4	318	2	CQ430441	CQ430441 Sequence
c 43	253.6	66.9	1197	5	AY696295	AY696295 Homo sapi
44	235.2	62.1	444	2	CQ505007	CQ505007 Sequence
45	235.2	62.1	444	2	CQ510749	CQ510749 Sequence

ALIGNMENTS

RESULT 1
CS110385
LOCUS

CS110385

379 bp

DNA

linear

PAT 22-JUN-2005

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 02:54:23 ; Search time 3144 Seconds
(without alignments)
6740.912 Million cell updates/sec

Title: US-10-010-742-52
Perfect score: 379
Sequence: 1 acttttgccaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	154.6	40.8	770	2	BI913122	BI913122 603179852
c 2	154.6	40.8	1335	14	AY408468	AY408468 Homo sapi
c 3	149.2	39.4	559	9	DA362614	DA362614 DA362614
c 4	141	37.2	623	1	AA193450	AA193450 zr40e07.r
c 5	140.4	37.0	1329	14	AY408470	AY408470 Mus muscu
c 6	140.4	37.0	3860	6	AK038526	AK038526 Mus muscu
c 7	128.6	33.9	628	4	BX272921	BX272921 BX272921
c 8	128.6	33.9	651	4	BX267843	BX267843 BX267843
c 9	128.6	33.9	676	5	CD216415	CD216415 pgp2n.pk0
c 10	125.6	33.1	786	5	CF547569	CF547569 AGENCOURT
c 11	124	32.7	869	10	DR860522	DR860522 JGI_CABG5
c 12	124	32.7	874	9	CX967511	CX967511 JGI_CAAP2
c 13	124	32.7	1642	6	BC054308	BC054308 Xenopus l
c 14	121	31.9	567	7	BF509149	BF509149 UI-H-BI4-
c 15	119.8	31.6	218	11	AY758967	AY758967 CH255-13m
c 16	119.8	31.6	556	5	CD734809	CD734809 4048891 1
c 17	119.2	31.5	735	3	BU243372	BU243372 603778833
c 18	118.2	31.2	839	3	BU227845	BU227845 603947881
c 19	116.6	30.8	824	9	CX966129	CX966129 JGI_CAAP1
c 20	116	30.6	792	2	BG193485	BG193485 RST12619
c 21	115.2	30.4	767	5	CJ023895	CJ023895 CJ023895
c 22	115	30.3	655	2	BJ909012	BJ909012 BJ909012
c 23	114.4	30.2	817	10	DR860523	DR860523 JGI_CABG5
c 24	114	30.1	773	2	BG461834	BG461834 RST44771
c 25	112	29.6	740	3	BP435575	BP435575 BP435575
c 26	112	29.6	813	3	BP435822	BP435822 BP435822
c 27	112	29.6	841	5	CJ025855	CJ025855 CJ025855
c 28	112	29.6	870	5	CJ022965	CJ022965 CJ022965
c 29	112	29.6	932	3	BQ881161	BQ881161 AGENCOURT
c 30	111.4	29.4	769	4	CA487879	CA487879 AGENCOURT
c 31	111.4	29.4	1038	2	BG291597	BG291597 602388704
c 32	111.2	29.3	252	2	BG204180	BG204180 RST23576
c 33	110.4	29.1	808	5	CJ022616	CJ022616 CJ022616
c 34	109.6	28.9	741	4	CB599980	CB599980 AGENCOURT
c 35	109.6	28.9	759	4	CB950823	CB950823 AGENCOURT
c 36	109.6	28.9	779	4	CB600740	CB600740 AGENCOURT
c 37	108.8	28.7	735	5	CK471537	CK471537 AGENCOURT
c 38	108.8	28.7	746	5	CK364271	CK364271 AGENCOURT
c 39	108.8	28.7	805	10	DR428109	DR428109 naw50f07.
c 40	108.8	28.7	864	8	CO554538	CO554538 AGENCOURT
c 41	108	28.5	570	4	CB601086	CB601086 AGENCOURT
c 42	108	28.5	622	2	BG971712	BG971712 602838239
c 43	108	28.5	640	2	BG971106	BG971106 602837813
c 44	108	28.5	651	7	BE851329	BE851329 uw94g07.y
c 45	108	28.5	747	4	CB953130	CB953130 AGENCOURT

ALIGNMENTS

RESULT 1
BI913122/c

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20070109_163108_us-10-010-742-52.rnj.**

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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 03:39:33 ; Search time 144 Seconds
(without alignments)
4924.654 Million cell updates/sec

Title: US-10-010-742-52
Perfect score: 379
Sequence: 1 actttgccaaagcagtaaagg.....ttcaggtatgagtcacagqqt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database :      Issued_Patents_NA:*
1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	154.6	40.8	1508	3	US-09-799-451-109	Sequence 109, App
c 2	154.6	40.8	2071	3	US-10-104-047-720	Sequence 720, App
c 3	154.6	40.8	2327	3	US-09-852-067-1	Sequence 1, Appli
c 4	154.6	40.8	2327	3	US-10-338-691-1	Sequence 1, Appli
c 5	153	40.4	1718	3	US-09-799-451-420	Sequence 420, App
c 6	111.4	29.4	2084	3	US-09-023-655-1045	Sequence 1045, Ap
c 7	98.4	26.0	2382	3	US-09-023-655-1436	Sequence 1436, Ap
c 8	96.8	25.5	2576	4	US-09-880-107-2138	Sequence 2138, Ap
c 9	82.6	21.8	1763	4	US-09-880-107-1610	Sequence 1610, Ap
c 10	73.4	19.4	300	3	US-09-172-108-2	Sequence 2, Appli
c 11	73.4	19.4	300	3	US-09-172-711-3	Sequence 3, Appli
c 12	69.8	18.4	1634	5	US-10-114-270-59	Sequence 59, Appl
c 13	69.8	18.4	1669	3	US-09-976-594-532	Sequence 532, App
c 14	66.6	17.6	2227	3	US-09-023-655-1433	Sequence 1433, Ap
c 15	66.4	17.5	888	3	US-09-023-655-198	Sequence 198, App
c 16	66.4	17.5	1676	3	US-09-991-181-263	Sequence 263, App
c 17	66.4	17.5	1676	3	US-09-990-444-263	Sequence 263, App
c 18	66.4	17.5	1676	3	US-09-997-333-263	Sequence 263, App
c 19	66.4	17.5	1676	3	US-09-992-598-263	Sequence 263, App
c 20	66.4	17.5	1676	4	US-09-989-735-263	Sequence 263, App
c 21	66.4	17.5	1676	5	US-09-989-726-263	Sequence 263, App
c 22	66.4	17.5	1676	5	US-09-997-514-263	Sequence 263, App
c 23	66.4	17.5	1676	5	US-09-989-728-263	Sequence 263, App
c 24	66.4	17.5	1676	5	US-09-997-349-263	Sequence 263, App
c 25	66.4	17.5	1676	5	US-09-997-653-263	Sequence 263, App
c 26	66.4	17.5	1676	5	US-09-989-293A-263	Sequence 263, App
c 27	66.4	17.5	2412	3	US-10-104-047-824	Sequence 824, App
c 28	65	17.2	2073	3	US-09-023-655-1385	Sequence 1385, Ap
c 29	65	17.2	2073	4	US-09-880-107-1601	Sequence 1601, Ap
c 30	65	17.2	2369	4	US-09-880-107-3277	Sequence 3277, Ap
c 31	65	17.2	5050	3	US-09-949-016-132	Sequence 132, App
c 32	64.4	17.0	31208	3	US-09-852-067-3	Sequence 3, Appli
c 33	64.4	17.0	31208	3	US-10-338-691-3	Sequence 3, Appli
c 34	64.2	16.9	1185	3	US-09-023-655-1270	Sequence 1270, Ap
c 35	64.2	16.9	2367	3	US-09-949-016-4207	Sequence 4207, Ap
36	55.2	14.6	285	3	US-09-020-956-153	Sequence 153, App
37	55.2	14.6	285	3	US-09-030-607-153	Sequence 153, App
38	55.2	14.6	285	3	US-09-439-313-153	Sequence 153, App
39	55.2	14.6	285	3	US-09-352-616A-153	Sequence 153, App
40	55.2	14.6	285	3	US-09-232-149A-153	Sequence 153, App
41	55.2	14.6	285	3	US-09-159-812-153	Sequence 153, App
42	55.2	14.6	285	3	US-09-636-215-153	Sequence 153, App
43	55.2	14.6	285	3	US-09-685-166A-153	Sequence 153, App
44	55.2	14.6	285	3	US-09-115-453-153	Sequence 153, App
45	55.2	14.6	285	3	US-09-688-489-153	Sequence 153, App

ALIGNMENTS

RESULT 1

US-09-799-451-109/c

; Sequence 109, Application US/09799451

; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

SCORE Search Results Details for Application 10010742 and Search Result 20070109_163111_us-10-010-742-52.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 04:32:09 ; Search time 924 Seconds
(without alignments)
5040.058 Million cell updates/sec

Title: US-10-010-742-52
Perfect score: 379
Sequence: 1 acttttgccaagcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	379	100.0	379	3	US-09-778-320-52	Sequence 52, Appl
	2	379	100.0	379	3	US-09-910-689-52	Sequence 52, Appl
	3	379	100.0	379	6	US-10-010-742-52	Sequence 52, Appl
	4	379	100.0	379	8	US-10-714-389-52	Sequence 52, Appl
	5	379	100.0	379	8	US-10-717-296-52	Sequence 52, Appl
c	6	379	100.0	598	9	US-10-357-930-24431	Sequence 24431, A
c	7	379	100.0	598	9	US-10-357-930-28061	Sequence 28061, A
c	8	379	100.0	870	6	US-10-198-846-4883	Sequence 4883, App
c	9	379	100.0	963	3	US-09-910-689-303	Sequence 303, App
c	10	379	100.0	963	6	US-10-010-742-303	Sequence 303, App
c	11	379	100.0	963	8	US-10-717-296-303	Sequence 303, App
c	12	379	100.0	1299	6	US-10-198-846-10784	Sequence 10784, A
c	13	379	100.0	1518	3	US-09-910-689-305	Sequence 305, App
c	14	379	100.0	1518	6	US-10-010-742-305	Sequence 305, App
c	15	379	100.0	1518	6	US-10-067-668-3	Sequence 3, Appli
c	16	379	100.0	1518	6	US-10-175-696-3	Sequence 3, Appli
c	17	379	100.0	1518	8	US-10-776-871-3	Sequence 3, Appli
c	18	379	100.0	1518	8	US-10-717-296-305	Sequence 305, App
c	19	379	100.0	1548	8	US-10-717-296-312	Sequence 312, App
c	20	379	100.0	1586	8	US-10-181-108-35	Sequence 35, Appl
c	21	379	100.0	1586	13	US-11-079-743-35	Sequence 35, Appl
c	22	379	100.0	1598	3	US-09-910-689-302	Sequence 302, App
c	23	379	100.0	1598	6	US-10-010-742-302	Sequence 302, App
c	24	379	100.0	1598	8	US-10-717-296-302	Sequence 302, App
c	25	379	100.0	1894	8	US-10-058-270A-1	Sequence 1, Appli
c	26	379	100.0	1975	6	US-10-067-668-1	Sequence 1, Appli
c	27	379	100.0	1975	6	US-10-175-696-1	Sequence 1, Appli
c	28	379	100.0	1975	8	US-10-776-871-1	Sequence 1, Appli
c	29	379	100.0	2015	3	US-09-910-689-304	Sequence 304, App
c	30	379	100.0	2015	6	US-10-010-742-304	Sequence 304, App
c	31	379	100.0	2015	8	US-10-296-606-23	Sequence 23, Appl
c	32	379	100.0	2015	8	US-10-717-296-304	Sequence 304, App
c	33	379	100.0	2020	6	US-10-227-884-29	Sequence 29, Appl
c	34	379	100.0	2020	6	US-10-230-163-29	Sequence 29, Appl
c	35	379	100.0	2020	6	US-10-230-338-29	Sequence 29, Appl
c	36	379	100.0	2020	6	US-10-218-631-29	Sequence 29, Appl
c	37	379	100.0	2020	6	US-10-230-414-29	Sequence 29, Appl
c	38	379	100.0	2020	6	US-10-232-224-29	Sequence 29, Appl
c	39	379	100.0	2020	6	US-10-216-159A-29	Sequence 29, Appl
c	40	379	100.0	2020	6	US-10-218-849-29	Sequence 29, Appl
c	41	379	100.0	2020	6	US-10-227-873-29	Sequence 29, Appl
c	42	379	100.0	2020	6	US-10-227-883-29	Sequence 29, Appl
c	43	379	100.0	2020	6	US-10-219-076-29	Sequence 29, Appl
c	44	379	100.0	2020	6	US-10-230-434-29	Sequence 29, Appl
c	45	379	100.0	2020	6	US-10-219-003-29	Sequence 29, Appl

ALIGNMENTS

SCORE Search Results Details for Application 10010742 and Search Result 20070109_163115_us-10-010-742-52.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 04:34:33 ; Search time 726 Seconds
(without alignments)
1422.648 Million cell updates/sec

Title: US-10-010-742-52
Perfect score: 379
Sequence: 1 acttttgccaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3650718 seqs, 1362588608 residues

Total number of hits satisfying chosen parameters: 7301436

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	379	100.0	1906	6	US-10-540-310-3	Sequence 3, Appli
c	2	363	95.8	2608	8	US-11-293-697-1857	Sequence 1857, Ap
c	3	154.6	40.8	1555	8	US-11-266-748A-367721	Sequence 367721,
	4	154.6	40.8	1555	8	US-11-266-748A-451100	Sequence 451100,
c	5	154.6	40.8	2343	6	US-10-131-833A-107	Sequence 107, App
c	6	154.6	40.8	2349	8	US-11-293-697-2301	Sequence 2301, Ap
c	7	154.6	40.8	2382	8	US-11-266-748A-56478	Sequence 56478, A
	8	154	40.6	1000	8	US-11-266-748A-203310	Sequence 203310,
	9	154	40.6	1000	8	US-11-266-748A-283212	Sequence 283212,
c	10	154	40.6	1000	8	US-11-266-748A-309852	Sequence 309852,
	11	154	40.6	1000	8	US-11-266-748A-392920	Sequence 392920,
c	12	154	40.6	1000	8	US-11-266-748A-483638	Sequence 483638,
	13	154	40.6	193471	8	US-11-266-748A-23901	Sequence 23901, A
c	14	114.4	30.2	2376	8	US-11-293-697-2332	Sequence 2332, Ap
c	15	111.4	29.4	1539	7	US-11-371-354-5351	Sequence 5351, Ap
c	16	111.4	29.4	1539	7	US-11-371-354-60240	Sequence 60240, A
c	17	111.4	29.4	1558	8	US-11-266-748A-78471	Sequence 78471, A
	18	111.4	29.4	1558	8	US-11-266-748A-131282	Sequence 131282,
c	19	111.4	29.4	2147	10	US-11-090-997-1025	Sequence 1025, Ap
c	20	108	28.5	1871	10	US-11-090-997-135	Sequence 135, App
c	21	108	28.5	1871	10	US-11-397-327-38	Sequence 38, Appl
	22	100.4	26.5	1754	8	US-11-266-748A-361338	Sequence 361338,
c	23	100.4	26.5	1754	8	US-11-266-748A-444717	Sequence 444717,
c	24	98.4	26.0	1000	8	US-11-266-748A-394439	Sequence 394439,
	25	98.4	26.0	1000	8	US-11-266-748A-465485	Sequence 465485,
c	26	96.8	25.5	1368	7	US-11-371-354-6869	Sequence 6869, Ap
c	27	96.8	25.5	1368	7	US-11-371-354-64400	Sequence 64400, A
c	28	95.2	25.1	779	8	US-11-266-748A-262386	Sequence 262386,
	29	95.2	25.1	779	8	US-11-266-748A-322903	Sequence 322903,
c	30	94	24.8	877	8	US-11-266-748A-214290	Sequence 214290,
c	31	93	24.5	1000	8	US-11-266-748A-293498	Sequence 293498,
	32	93	24.5	1000	8	US-11-266-748A-344927	Sequence 344927,
	33	89	23.5	600	8	US-11-266-748A-102267	Sequence 102267,
c	34	89	23.5	600	8	US-11-266-748A-155078	Sequence 155078,
	35	79.8	21.1	947	8	US-11-266-748A-186910	Sequence 186910,
c	36	79.8	21.1	947	8	US-11-266-748A-241605	Sequence 241605,
c	37	75	19.8	2608	8	US-11-293-697-1514	Sequence 1514, Ap
c	38	69.8	18.4	1575	7	US-11-371-354-55428	Sequence 55428, A
c	39	69.8	18.4	2950	8	US-11-266-748A-24706	Sequence 24706, A
c	40	66.6	17.6	2227	10	US-11-414-896A-1	Sequence 1, Appli
c	41	66.6	17.6	2360	8	US-11-266-748A-57526	Sequence 57526, A
c	42	66.4	17.5	1000	8	US-11-266-748A-402012	Sequence 402012,
	43	66.4	17.5	1000	8	US-11-266-748A-473058	Sequence 473058,
c	44	66.4	17.5	1575	7	US-11-371-354-65796	Sequence 65796, A
c	45	66.4	17.5	1676	6	US-10-196-749-203	Sequence 203, App

ALIGNMENTS

RESULT 1

US-10-540-310-3/c

; Sequence 3, Application US/10540310

; Publication No. US20060166212A1

; GENERAL INFORMATION: